IFWO

RAW SEQUENCE LISTING   DATE: 08/30/2004
PATENT APPLICATION: US/10/777,789   TIME: 14:51:54

     Input Set : N:\Crf3\RULE60\10777789.raw.txt
     Output Set: N:\CRF4\08302004\J777789.raw

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 1 <110> APPLICANT: Oppmann, Birgit
 2        Timans, Jacqueline C.
 3        Kastelein, Robert A.
 4        Bazan, J. Fernando
 5 <120> TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
 6 <130> FILE REFERENCE: DX0935K
 7 <140> CURRENT APPLICATION NUMBER: US/10/777,789
 8 <141> CURRENT FILING DATE: 2004-02-11
 9 <150> PRIOR APPLICATION NUMBER: US/09/521,335
10 <151> PRIOR FILING DATE: 2000-03-09
11 <160> NUMBER OF SEQ ID NOS: 13
12 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 1790
16 <212> TYPE: DNA
17 <213> ORGANISM: primate
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19 <221> NAME/KEY: CDS
20 <222> LOCATION: (162)..(806)
21 <220> FEATURE:
22 <221> NAME/KEY: mat_peptide
23 <222> LOCATION: (213)..(806)
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26      ccgcggctcg ccctcccact ccgccagcct ccgggagagg agccgcaccc ggccggcccg 120
27      gccccagccc catggacctc cgagcagggg actcgtgggg g atg tta gcg tgc ctg 176
28                                                    Met Leu Ala Cys Leu
29                                                           -15
30      tgc acg gtg ctc tgg cac ctc cct gca gtg cca gct ctc aat cgc aca    224
31      Cys Thr Val Leu Trp His Leu Pro Ala Val Pro Ala Leu Asn Arg Thr
32              -10                 -5                  -1  1
33      ggg gac cca ggg cct ggc ccc tcc atc cag aaa acc tat gac ctc acc    272
34      Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys Thr Tyr Asp Leu Thr
35        5                  10                  15                  20
36      cgc tac ctg gag cac caa ctc cgc agc ttg gct ggg acc tat ctg aac    320
37      Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala Gly Thr Tyr Leu Asn
38                      25                  30                  35
39      tac ctg ggc ccc cct ttc aac gag cca gac ttc aac cct ccc cgc ctg    368
40      Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe Asn Pro Pro Arg Leu
41                  40                  45                  50
42      ggg gca gag act ctg ccc agg gcc act gtt gac ttg gag gtg tgg cga    416
43      Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asp Leu Glu Val Trp Arg
44                  55                  60                  65
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46      Ser Leu Asn Asp Lys Leu Arg Leu Thr Gln Asn Tyr Glu Ala Tyr Ser
47           70                  75                  80
48      cac ctt ctg tgt tac ttg cgt ggc ctc aac cgt cag gct gcc act gct   512
49      His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg Gln Ala Ala Thr Ala
50        85                  90                  95                 100
51      gag ctg cgc cgc agc ctg gcc cac ttc tgc acc agc ctc cag ggc ctg   560
52      Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr Ser Leu Gln Gly Leu
53                  105                 110                 115
54      ctg ggc agc att gcg ggc gtc atg gca gct ctg ggc tac cca ctg ccc   608
55      Leu Gly Ser Ile Ala Gly Val Met Ala Ala Leu Gly Tyr Pro Leu Pro
56                  120                 125                 130
57      cag ccg ctg cct ggg act gaa ccc act tgg act cct ggc cct gcc cac   656
58      Gln Pro Leu Pro Gly Thr Glu Pro Thr Trp Thr Pro Gly Pro Ala His
59                  135                 140                 145
60      agt gac ttc ctc cag aag atg gac gac ttc tgg ctg ctg aag gag ctg   704
61      Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp Leu Leu Lys Glu Leu
62                  150                 155                 160
63      cag acc tgg ctg tgg cgc tcg gcc aag gac ttc aac cgg ctc aag aag   752
64      Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe Asn Arg Leu Lys Lys
65      165                 170                 175                 180
66      aag atg cag cct cca gca gct gca gtc acc ctg cac ctg ggg gct cat   800
67      Lys Met Gln Pro Pro Ala Ala Ala Val Thr Leu His Leu Gly Ala His
68                  185                 190                 195
69      ggc ttc tgacttctga ccttctcctc ttcgctcccc cttcaaaccc tgctcccact   856
70      Gly Phe
72      ttgtgagagc cagccctgta tgccaacacc tgttgagcca ggagacagaa gctgtgagcc 916
73      tctggccctt tcctggaccg gctgggcgtg tgatgcgatc agccctgtct cctccccacc 976
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80      tggggtctgc attggaggtg ccctataaac cagaagagaa aatactgaaa gcacaggggc 1396
81      agggacagac cagaccagac ccaggagtct ccaaagcaca gagtggcaaa caaaacccga 1456
82      gctgagcatc aggaccttgc ctcgaattgt cttccagtat tacggtgcct cttctctgcc 1516
83      cccttttccca gggtatctgt gggttgccag gctggggagg gcaaccatag ccacaccaca 1576
84      ggatttcctg aaagtttaca atgcagtagc attttggggt gtagggtggc agctccccaa 1636
85      ggccctgccc cccagcccca cccactcatg actctaagtg tgttgtatta atatttattt 1696
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91 <212> TYPE: PRT
92 <213> ORGANISM: primate
93 <400> SEQUENCE: 2
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97         -1   1               5                  10                  15
98        Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
99                        20                  25                  30
100        Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
101                    35                  40                  45
102        Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asp
103                    50                  55                  60
104        Leu Glu Val Trp Arg Ser Leu Asn Asp Lys Leu Arg Leu Thr Gln Asn
105             65                  70                  75
106        Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
107         80                  85                  90                  95
108        Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
109                        100                 105                 110
110        Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Ala Leu
111                    115                 120                 125
112        Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Thr Trp Thr
113                    130                 135                 140
114        Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
115             145                 150                 155
116        Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
117         160                 165                 170                 175
118        Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ala Val Thr Leu
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120        His Leu Gly Ala His Gly Phe
121                    195
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124  <211> LENGTH: 648
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126  <213> ORGANISM: primate
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132  <222> LOCATION: (52)..(645)
133  <400> SEQUENCE: 3
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135     Met Leu Ala Cys Leu Cys Thr Val Leu Trp His Leu Pro Ala Val Pro
136              -15                 -10                  -5
137     gct ctt aat cgc aca gga gat cca ggc cct ggc ccc tcc atc cag aaa      96
138     Ala Leu Asn Arg Thr Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys
139      -1   1               5                  10                  15
140     acc tat gac ctc acc cgc tac ctg gag cat caa ctc cgc agc tta gct     144
141     Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
142                     20                  25                  30
143     ggg acc tac ctg aac tac ctg ggg ccc cct ttc aac gag cct gac ttc     192
144     Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
145                 35                  40                  45
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146        aat cct cct cga ctg ggg gca gaa act ctg ccc agg gcc acg gtc aac    240
147        Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asn
148                50                  55                  60
149        ttg gaa gtg tgg cga agc ctc aat gac agg ctg cgg ctg acc cag aac    288
150        Leu Glu Val Trp Arg Ser Leu Asn Asp Arg Leu Arg Leu Thr Gln Asn
151            65                  70                  75
152        tat gag gcg tac agt cac ctc ctg tgt tac ttg cgt ggc ctc aac cgt    336
153        Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
154        80                  85                  90                  95
155        cag gct gcc aca gct gaa ctc cga cgt agc ctg gcc cac ttc tgt acc    384
156        Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
157                100                 105                 110
158        agc ctc cag ggc ctg ctg ggc agc att gca ggt gtc atg gcg acg ctt    432
159        Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Thr Leu
160                115                 120                 125
161        ggc tac cca ctg ccc cag cct ctg cca ggg act gag cca gcc tgg gcc    480
162        Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Ala Trp Ala
163                130                 135                 140
164        cct ggc cct gcc cac agt gac ttc ctc cag aag atg gat gac ttc tgg    528
165        Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
166            145                 150                 155
167        ctg ctg aag gag ctg cag acc tgg cta tgg cgt tca gcc aag gac ttc    576
168        Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
169        160                 165                 170                 175
170        aac cgg ctt aag aag aag atg cag cct cca gca gct tca gtc acc ctg    624
171        Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ser Val Thr Leu
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174        His Leu Glu Ala His Gly Phe
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185        -1   1               5                  10                  15
186        Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
187                20                  25                  30
188        Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
189                35                  40                  45
190        Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asn
191                50                  55                  60
192        Leu Glu Val Trp Arg Ser Leu Asn Asp Arg Leu Arg Leu Thr Gln Asn
193            65                  70                  75
194        Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
195        80                  85                  90                  95
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196        Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
197                        100                 105                 110
198        Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Thr Leu
199                        115                 120                 125
200        Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Ala Trp Ala
201                        130                 135                 140
202        Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
203                        145                 150                 155
204        Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
205        160                 165                 170                 175
206        Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ser Val Thr Leu
207                        180                 185                 190
208        His Leu Glu Ala His Gly Phe
209                        195
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212 <211> LENGTH: 203
213 <212> TYPE: PRT
214 <213> ORGANISM: rodent
215 <400> SEQUENCE: 5
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218        His Trp Lys His Gly Ala Gly Ser Pro Leu Pro Ile Thr Pro Val Asn
219                         20                 25                 30
220        Ala Thr Cys Ala Ile Arg His Pro Cys His Gly Asn Leu Met Asn Gln
221                         35                 40                 45
222        Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe
223                  50                 55                 60
224        Ile Ser Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu
225           65                 70                 75                 80
226        Lys Leu Cys Ala Pro Asn Met Thr Asp Phe Pro Ser Phe His Gly Asn
227                         85                 90                 95
228        Gly Thr Glu Lys Thr Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr
229                        100                 105                 110
230        Leu Ser Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn
231                        115                 120                 125
232        Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr Ile Asp Val
233                        130                 135                 140
234        Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Asn Lys Tyr
235        145                 150                 155                 160
236        Arg Val Gly His Val Asp Val Pro Pro Val Pro Asp His Ser Asp Lys
237                        165                 170                 175
238        Glu Ala Phe Gln Arg Lys Lys Leu Gly Cys Gln Leu Leu Gly Thr Tyr
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245 <212> TYPE: PRT
246 <213> ORGANISM: primate
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